

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:20:15 ; Search time 45.33 Seconds

(without alignments)
165.342 Million cell updates/sec

Title: US-09-351-778A-9

Perfect score: 1 MTSSTAPPTDYKNTATGL.....ICLKKRRRAPPYRIIVL 78

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 28338 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28338

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR.71:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	30.8	93	1 ERAD53	early E3A 10.5K pr
2	7	9.0	160	2 C95415	hypothetical prote
3	7	9.0	197	2 C86523	CT142 hypothetical
4	7	9.0	387	2 C89783	hypothetical prote
5	7	9.0	391	2 D97201	alCAR transformati
6	7	9.0	425	2 AC2909	MFS permease [impo
7	7	9.0	487	2 B87684	probable lactate
8	7	9.0	536	2 T27668	hypothetical prote
9	7	9.0	965	2 T17395	probable DEAH ATP-
10	7	9.0	1175	2 H83437	hypothetical prote
11	7	9.0	69	2 P40453	adenylate cyclase
12	7	7.7	89	2 D87338	hypothetical prote
13	7	7.7	94	2 E82629	phage-related prot
14	7	7.7	94	2 D82626	phage-related prot
15	7	7.7	97	2 T40639	hypothetical prote
16	7	7.7	113	2 C81280	hypothetical prote
17	7	7.7	113	2 G81990	hypothetical prote
18	7	7.7	119	2 H83186	hypothetical prote
19	7	7.7	121	1 J01646	nucleic acid-bind
20	7	7.7	126	2 D95915	hypothetical prote
21	7	7.7	128	2 AD1054	conserved hypochet
22	7	7.7	130	2 E70353	hypothetical prote
23	7	7.7	134	2 S52546	thionin variant th
24	7	7.7	136	2 T23996	hypothetical prote
25	7	7.7	142	2 S32960	hypothetical prote
26	7	7.7	144	2 AC3388	high-affinity bran
27	7	7.7	148	2 T03569	hypothetical 16.9K
28	7	7.7	150	2 G87270	general secretion
29	7	7.7	157	2 S75191	hypothetical prote

30	6	7.7	157	2 S35037	heliX-loop-heliX p
31	6	7.7	157	2 T48683	hypothetical prote
32	6	7.7	170	2 T17286	hypothetical prote
33	6	7.7	174	2 C82129	conserved hypochet
34	6	7.7	182	2 H87383	hypothetical prote
35	6	7.7	211	2 T36878	hypothetical prote
36	6	7.7	216	2 S29712	segmentation prote
37	6	7.7	222	2 A75476	response regulator
38	6	7.7	224	2 H82658	carboxylesterase X
39	6	7.7	230	2 T51265	probable HLH DNA b
40	6	7.7	248	1 Q0BE4L	conserved glycoprot
41	6	7.7	263	1 B64328	conserved hypochet
42	6	7.7	279	2 A72102	conserved hypochet
43	6	7.7	279	2 G86522	CT142 hypothetical
44	6	7.7	280	2 A53027	transcription fact
45	6	7.7	281	2 S36748	transcription fact

ALIGNMENTS

RESULT 1

ERAD53

early E3A 10.5K protein - human adenovirus 5

C:Species: Mastadenovirus h5 (human adenovirus 5)

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999

C:Accession: A05245

R:Cladarias, C.; Wold, W.S.M.

Virology 140, 28-43, 1985

A:Title: DNA sequence of the early E3 transcription unit of adenovirus 5.

A:Reference number: A94335; MUID:85092388

A:Accession: A05245

A:Molecule type: DNA

A:Residues: 1-93 <CLAS>

A:Cross-references: GB:X03002; NID:958503; PIDN:CAA26784.1; PID:958507

C:Superfamily: adenovirus early E3A 10.5K protein

C:Keywords: early protein; transmembrane protein

Query Match 30.8% Score 24; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.2e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMFSLMFEVCLIMMLICLKR 64
DB 34 MMFSLMFEVCLIMMLICLKR 57

RESULT 2

C95415

hypothetical protein S8a2279 [Imported] - Sinorhizobium meliloti (strain 1021) magap1

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: C95415

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B

: Kalmann, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wellis, D.H.; Yeh, K

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: C95415

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK65885.1; PID:g14524394; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Flann, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalmann, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeJau

hebaull, P.; Vandemol, M.; Vornholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMA2279
 A:Genome: Plasmid

Query Match 9.0%; Score 7; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 |||||||
 Db 28 TGSTIAP 34

RESULT 3
 C86523
 CT12 hypothetical protein_2 [imported] - Chlamydomonas pneumoniae (strain J138)
 C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: C86523
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Uuchi, K.; Shiba, T.; Is
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349
 A:Accession: C86523
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-197 <STO>
 A:Cross-references: GB:BA000008; NID:98978632; PIDN:BA98469.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPJ0259

Query Match 9.0%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||||
 Db 74 ATGLTSA 80

RESULT 4
 C89783
 Hypothetical protein SA0200 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89783
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89783
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-387 <UR>
 A:Cross-references: GB:BA000018; PID:g13700123; PIDN:BA841422.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA0200

Query Match 9.0%; Score 7; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 20 LTSLNL 26
 |||||||

Db 27 LTSLNL 33

RESULT 5
 D97201
 AICAR transformylase domain of PurH-like protein [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: D97201
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markovova, K.S.; Zeng, Q.; Gibson, R.; L
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97201
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <UR>
 A:Cross-references: GB:AE001437; PIDN:AAK80399.1; PID:g15025462; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC2445

Query Match 9.0%; Score 7; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||||
 Db 58 ATGLTSA 64

RESULT 6
 AC2909
 MFS permease [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AC2909
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; MCCI
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kem
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AC2909
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-425 <UR>
 A:Cross-references: GB:AE008688; PIDN:AL43689.1; PID:g17741216; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu2708
 A:Map position: circular chromosome

Query Match 9.0%; Score 7; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 |||||||
 Db 390 TGSTIAP 396

RESULT 7
 B97684
 probable taurate transporter AGR_C_4908 [imported] - Agrobacterium tumefaciens (stra
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: B97684

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A:Reference number: A97359; PMID:11743194
 A:Accession: B97684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-487 <KIR>
 A:Cross-references: GB:AE007869; PIDN:915157922; GSPDB:GN00169
 A:Gene: AGR_C_4908
 A:Map position: circular chromosome

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 487;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGSTAP 8
 |||||
 DB 452 TGSTAP 458

RESULT 8
 T27668
 hypothetical protein ZK1053.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T27668
 R:Kershaw, J.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: 220402
 A:Accession: T27668
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-536 <WIL>
 A:Cross-references: EMBL:282084; PIDN:CA804976.1; GSPDB:GN00019; CESP:ZK1053.2
 A:Experimental source: clone ZK1053
 C:Genetics:
 A:Gene: CESP:ZK1053.2
 A:Map position: 1
 A:Introns: 56/3: 88/3: 203/1: 228/2: 383/1: 467/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK1053.2

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 536;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 STIAPT 10
 |||||
 DB 295 STIAPT 301

RESULT 9
 T17395
 probable DEAH ATP-dependent helicase - *Dichelobacter nodosus*
 C:Species: *Dichelobacter nodosus*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17395
 R:Billington, S.J.; Huggins, A.S.; Johnsen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, M.; Infect. Immun. 67, 1277-1286, 1999
 A:Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) C
 A:Reference number: 218734; PMID:99150261
 A:Accession: T17395
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-965 <BIL>
 A:Cross-references: EMBL:U20246; NID:93493323; PID:9317808; PIDN:ACG3384.1
 A:Experimental source: strain A198

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 965;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ALNPOV 29
 |||||
 DB 772 ALNPOV 778

RESULT 10
 H83437
 hypothetical protein PA1669 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83437
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; L.; Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A:Reference number: A82950; PMID:20437337
 A:Accession: H83437
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1175 <STO>
 A:Cross-references: GB:AE004594; GB:AE004091; NID:99947630; PIDN:ANG05038.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1669

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 1175;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 KRRRAP 69
 |||||
 DB 213 KRRRAP 219

RESULT 11
 P0453
 adenylate cyclase (EC 4.6.1.1) - human (fragment)
 N:Alternate names: adenyl cyclase
 C:Species: Homo sapiens (man)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: P0453
 R:Bellevue, K.; Yoshimura, M.; Kuo, M.; Hoffman, P.L.; Cooper, D.M.F.; Tabakoff, B.; Blochem. Biophys. Res. Commun. 192, 311-318, 1993
 A:Title: A novel adenyl cyclase sequence cloned from the human erythroleukemia cell
 A:Reference number: P0453; PMID:9336590
 A:Accession: P0453
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-69 <HEL>
 C:Comment: This enzyme catalyzes the synthesis of adenosin 3',5'-cyclic monophosphate
 C:Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology
 C:Keywords: phosphorus-oxygen lyase
 F:1-65/Domain: guanylate cyclase catalytic domain homology (fragment) <GCC>

Query Match
 Best Local Similarity 100.0%; Score 6; DB 2; Length 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 FSIALM 49
 |||||
 DB 28 FSIALM 33

RESULT 12
 D87338
 hypothetical protein CC0719 [imported] - *Caulobacter crescentus*

C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C/Accession: D87338
 R:Netman, M.C.; Deiblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolton, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259667
 A:Accession: D87338
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <STO>
 A:Cross-references: GB:AE005673; NID:g13421946; PIDN:AAK22704.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0719

Query Match 7.7%: Score 6; DB 2; Length 89;
 Best Local Similarity 100.0%: Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 RRRARP 69
 |||||
 Db 16 RRRARP 21

RESULT 13
 E82629
 phage-related protein XF1869 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: E82629
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 405, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: E82629
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-94 <SIM>
 A:Cross-references: GB:AE004007; GB:AE003849; NID:g9106944; PIDN:AAF84675.1; GSPDB:GN00148
 A:Experimental source: strain 9a5c
 R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigh, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, R. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsubako, M.H.; Vallada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1869

Query Match 7.7%: Score 6; DB 2; Length 94;
 Best Local Similarity 100.0%: Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 21 TSLNLT 26
 |||||
 Db 39 TSLNLT 44

RESULT 14
 D82626

phage-related protein XF1876 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: D82626
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-94 <SIM>
 A:Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84682.1; GSPDB:GN00148
 A:Experimental source: strain 9a5c
 R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw M: Tsubako, M.H.; Vallada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L. A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1876

Query Match 7.7%: Score 6; DB 2; Length 94;
 Best Local Similarity 100.0%: Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 21 TSLNLT 26
 |||||
 Db 39 TSLNLT 44

RESULT 15
 T40639
 hypothetical protein SPBC685.08 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T40639
 R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: 221928
 A:Accession: T40639
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-97 <SPB>
 A:Cross-references: EMBL:AL049474; PIDN:CA839365.1; GSPDB:GN00067; SPDB:SPBC685.08
 A:Experimental source: strain 972h-; cosmid C685
 A:Contents:
 C:Genetics:
 A:Gene: SPDB:SPBC685.08
 A:Map position: 2
 A:introns: 1/3

Query Match 7.7%: Score 6; DB 2; Length 97;
 Best Local Similarity 100.0%: Pred. No. 55;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 SALNLP 27
 |||||
 Db 32 SALNLP 37

Search completed: June 21, 2002, 08:21:53
Job time: 98 sec
